

**Amendments to the specification**

Please amend the paragraph bridging pages 21 and 22 with the following paragraph:

Similarly, in a particular embodiment, two amino acid sequences are “substantially homologous” or “substantially similar” when greater than 70% of the amino acids are identical, or greater than about 90% are similar (functionally similar). Preferably, the similar or homologous sequences are identified by alignment using, for example, the GCG (Genetics Computer Group, Program Manual for the GCG Package, *Version 7*, Madison, Wisconsin) pileup program, BLAST, and Clustal W analysis (MacVector). Sequence comparison algorithms can also be found at <http://www.nwfsc.noaa.gov/bioinformatics.html> [www.nwfsc.noaa.gov/bioinformatics.html](http://www.nwfsc.noaa.gov/bioinformatics.html).